This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (cancelled)

2. (cancelled)

3. (cancelled)

4. (cancelled)

5. (cancelled)

6. (cancelled)

7. (cancelled)

8. (cancelled)

9. (cancelled)

10. (cancelled)

11. (original) A method for removing or controlling errors in nucleic acid molecules comprising arbitrary user-specified sequence composition and length, the method comprising:

a) providing a plurality or pool of nucleic acid molecules synthesized to have a user-specified sequence and length; and,

b) selectively amplifying error-free nucleic acid molecules from said plurality or pool, thereby decreasing the relative amount of any nucleic acid molecules that contain errors.

12. (original) A method for removing or controlling errors in nucleic acid molecules comprising arbitrary user-specified sequence composition and length, the method comprising:

a) providing a plurality or pool of nucleic acid molecules synthesized to have a user-specified sequence and length; and

b) correcting errors in said plurality or pool using nucleic acid molecules in said plurality or pool as a template for nucleic acid repair.

13. (original) A method for removing or controlling errors in nucleic acid molecules comprising arbitrary user-specified sequence composition and length, the method comprising:

a) providing a plurality or pool of nucleic acid molecules synthesized to have a user-specified sequence and length; and

b) removing errors from portions of said nucleic acid molecules and recombining remaining portions of said nucleic acid molecules to yield nucleic acid molecules having an error-free sequence.

14. (new claim) The method of claim 11, further comprising the step of combining at least one error-containing nucleic acid molecule from said plurality or pool with at least one component that prevents amplification of the error-containing nucleic acid molecule.

15. (new claim) The method of claim 14, wherein the component is a mismatch binding protein.

16. (new claim) The method of claim 14, wherein the component is cross-linked to the error-containing nucleic acid molecule.

17. (new claim) The method of claim 14, wherein at least two components are cross-linked to each other.

18. (new claim) The method of claim 14, wherein at least one component is cross-linked to itself.

19. (new claim) The method of claim 14, wherein the component comprises more than one molecule.

20. (new claim) The method of claim 12, the step of correcting errors comprising the step of targeting errors via methylation and selective demethylation.

21. (new claim) The method of claim 12, the step of correcting errors comprising the step of mismatch recognition and cleavage.

22. (new claim) The method of claim 21, wherein the step of mismatch recognition and cleavage is performed by a resolvase, a single-stranded nuclease, or a combination of a mismatch binding protein and a nuclease.

23. (new claim) The method of claim 12, the step of correcting errors comprising the step of generating at least one repair template by disassociation and reassociation of single-stranded nucleic acid molecules.

24. (new claim) The method of claim 12, the step of correcting errors comprising the step of generating at least one repair template by strand invasion.

25. (new claim) The method of claim 12, wherein no entire nucleic acid molecules in the plurality or pool need be error-free.

26. (new claim) The method of claim 13, the step of removing errors comprising the step of mismatch recognition and cleavage.

27. (new claim) The method of claim 26, wherein the step of mismatch recognition and cleavage is performed by a resolvase, a single-stranded nuclease, or a combination of a mismatch binding protein and a nuclease.

28. (new claim) The method of claim 26, wherein the step of mismatch recognition and cleavage is performed by a single molecule.

29. (new claim) The method of claim 13, wherein the step of removing errors is performed by the separate action of a mismatch binding protein and a nuclease.

30. (new claim) The method of claim 13, wherein no nucleic acid molecules in the plurality or pool need be error-free.